ARE GENETICS AND GENOMICS HELPFUL TO IMPROVE FEED EFFICIENCY IN NILE TILAPIA *Oreochromis niloticus*?

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Introduction

Improving feed efficiency in aquaculture is crucial to develop a more sustainable aquaculture. Feeds represent 30 to 70% of the total production costs, and have major environmental and social impacts (de Verdal et al, 2017).

Until now, the contribution of genetic improvement to this goal has been hampered by the lack of efficient phenotyping methods and of accurate genetic parameters of feed conversion rate (FCR) in fish. Different methods have been used to measure individual FCR in fish, but all of them have pros and cons, i.e. the loss of social interactions between fish, the low repeatability of measurements, or the time needed to measure the phenotype. Indvidual FCR is a difficult trait to measure. Using genomic selection would help to reduce the phenotyping effort by phenotyping fish that are not the candidates to selection (training population). These phenotypes are needed to establish a genomic prediction equation for the selection candidates, thus potentially reducing the phenotyping effort with a higher accuracy. The aim of the present study was to 1/ estimate the genetic parameters of performance and feed efficiency traits and 2/ assess the potential of genomic selection for feed efficiency. The GIFT strain, selected for growth for more than 15 generations, of Nile tilapia *Oreochromis niloticus*, was used for this purpose.

Material and methods

Video assessment of feed intake (FI) on individual fish reared in groups was used to estimate the genetic parameters of growth traits (body weight gain, BWG), FI, FCR and relative FI ($FI.BW^{-1}$) on 1,000 fish from 40 pedigreed full-sib families of Nile tilapia. Juvenile fish (22.4 g) were evaluated during 13 consecutive meals over 7 days (de Verdal et al., 2018). Each phenotyped individual was genotyped using DarT-seq methodology. A total of 4930 SNPs were used after quality control. Heritability was estimated with a pedigree-based or a genomic approach. Five-fold cross validation was apllied using different methodologies: pedigree-BLUP (pBLUP), genomic BLUP (gBLUP), and single-step gBLUP (ss-gBLUP) and twoBayesian methods (Lasso and BayesC-π) to estimate the reliability of EBVs.

The BLUPF90 family of programs (Misztal et al, 2002) was used for all analyses except for the Bayesian methods where GS3 (Legarra et al, 2010) was used.

Results

As expected, heritability estimates revealed a genetic control for feed efficiency traits in tilapia. Pedigree- and genomic-based heritabilities were rather different for all traits (Table 1). Estimates were lower with genomic data for FI and $FI.BW^{-1}$ but higher for BWG and FCR.

Trait	Pedigree h^2	Genomic h^2
BWG	0.27 ± 0.08	0.37 ±0.06
FI	0.45 ±0.09	0.17 ±0.05
$FI.BW^{-1}$	0.31 ±0.001	0.19 ±0.06
FCR	0.32 ±0.11	0.59 ±0.06

Table 1 – Estimation of pedigree and genomic heritabilities ± S.E.

EBVs estimated with different methodologies (pBLUP, gBLUP, ss-gBLUP, Lasso and BayesC-) were compared to observed phenotypes for all traits. Results for FCR and FI corrected for fixed effects are shown in Figure 1. Globally, all correlations were close to the expected accuracy, whatever the trait. The EBVs of FI were the most accurately predicted, with 95 to 100% of the expected accuracy, for pBLUP and Lasso, respectively.

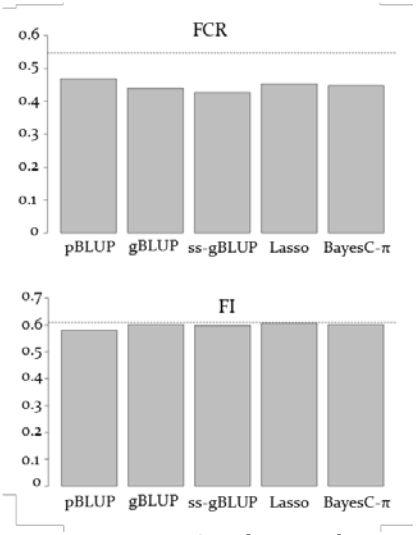

Figure 1 – Correlations between predicted EBVs for fish in the validation data in a given model (predicted from the training data) and the recorded FCR and FI. The dotted line represent the expected accuracy estimated using the equation of Daetwyler et al (2010).

Discussion and conclusions

Using this specific methodology to measure individual FI and estimate FCR, it is clear that genetic improvement of feed efficiency is possible in tilapia. These traits have moderate to high heritabilities. Genetic parameters estimates were not similar using the classical pedigree-based method and the genomic-based method, which can be partly explained by some intra-family effects, not visible using the pedigree-based estimations. The heritability estimates for FCR are relatively close to what was found by Besson et al (2019) in European sea bass, who estimated heritabilities of 0.25 and 0.47 for FCR (log transformed) using pedigree and genomic data, respectively. Regarding FI traits, the heritability drop could be explained by the relatively low number of SNPs used in the analyses, not all the QTLs being tracked by the SNPs.

We showed that accurate predictions of EBVs can be performed using different methodologies. According to the considered trait, the best methodology was not the same but accuracy differences between methodologies were rather small (less than 10%), and all methods were close to the expected accuracy. More genotypes and phenotypes might help increase the reliability of predictions and as a consequence, increase the impact of genomic selection on feed efficiency traits. Finally, although the heritability of FCR using genomic data was much higher than using pedigree data, the accurecy was very similar. As a consequence, using this number of SNPs and this measurement methodology, the clear advantage of using genomic data is reducing the phenotyping efforts, which can be useful knowing the complexity to measure FCR in fish.

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